

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Tryggvason, Karl  
Kestila, Marjo  
Lenkkeri, Ulla  
Mannikko, Minna

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(ii) TITLE OF INVENTION: Neph rin Gene and Protein

(iii) NUMBER OF SEQUENCES: 6

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
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(C) CITY: Chicago  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60606

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Chao, Mark  
(B) REGISTRATION NUMBER: 37,293  
(C) REFERENCE/DOCKET NUMBER: 97,842

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (312)913-0001  
(B) TELEFAX: (312)913-0002

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 4285 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: not relevant

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 1..66  
 (D) OTHER INFORMATION: /note= "putative signal peptide"

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..3723

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 67..3723

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 121..122  
 (D) OTHER INFORMATION: /note= "deletion mutation  
 FIN-Major"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 3800..3804  
 (D) OTHER INFORMATION: /note= "nonsense mutation in exon  
 26 FIN-Minor"

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 3178..3258  
 (D) OTHER INFORMATION: /note= "putative transmembrane  
 domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35	ATG GCC CTG GGG ACG ACG CTC AGG GCT TCT CTC CTG CTC CTG GGG CTG	48
	Met Ala Leu Gly Thr Thr Leu Arg Ala Ser Leu Leu Leu Leu Gly Leu	
	-22 -20 -15 -10	
40	CTG ACT GAA GGC CTG GCG CAG TTG GCG ATT CCT GCC TCC GTT CCC CGG	96
	Leu Thr Glu Gly Leu Ala Gln Leu Ala Ile Pro Ala Ser Val Pro Arg	
	-5 1 5 10	
45	GGC TTC TGG GCC CTG CCT GAA AAC CTG ACG GTG GTG GAG GGG GCC TCA	144
	Gly Phe Trp Ala Leu Pro Glu Asn Leu Thr Val Val Glu Gly Ala Ser	
	15 20 25	
50	GTG GAG CTG CGT TGT GGG GTC AGC ACC CCT GGC AGT GCG GTG CAA TGG	192
	Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp	
	30 35 40	
55	GCC AAA GAT GGG CTG CTC CTG GGC CCC GAC CCC AGG ATC CCA GGC TTC	240
	Ala Lys Asp Gly Leu Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe	
	45 50 55	
	CCG AGG TAC CGC CTG GAA GGG GAC CCT GCT AGA GGT GAA TTC CAC CTG	288
	Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu	

		60				65				70										
5	CAC His 75	ATC Ile	GAG Glu	GCC Ala	TGT Cys	GAC Asp 80	CTC Leu	AGC Ser	GAT Asp	GAC Asp	GCG Ala 85	GAG Glu	TAT Tyr	GAG Glu	TGC Cys	CAG Gln 90			336	
10	GTC Val	GGC Gly	CGC Arg	TCT Ser	GAG Glu 95	ATG Met	GGG Gly	CCC Pro	GAG Glu 100	CTC Leu	GTG Val	TCT Ser	CCC Pro	AGA Arg	GTG Val 105	ATC Ile			384	
15	CTC Leu	TCC Ser	ATC Ile	CTG Leu 110	GTT Val	CCT Pro	CCC Pro	AAG Lys	CTG Leu 115	CTC Leu	CTG Leu	CTG Leu	ACC Thr	CCA Pro 120	GAG Glu	GCA Ala			432	
20	GGC Gly	ACC Thr	ATG Met 125	GTC Val	ACC Thr	TGG Trp	GTA Val 130	GCT Ala	GGG Gly	CAG Gln	GAG Glu	TAC Tyr	GTG Val 135	GTC Val	AAC Asn	TGT Cys			480	
25	GTG Val	TCT Ser	GGG Gly	GAC Asp	GCG Ala	AAG Lys	CCA Pro 145	GCA Ala	CCT Pro	GAC Asp	ATC Ile	ACC Thr	ATT Ile	CTC Leu	CTG Leu	AGT Ser			528	
30	GGA Gly	CAG Gln	ACA Thr	ATA Ile	TCT Ser	GAC Asp 160	ATC Ile	TCT Ser	GCA Ala	AAC Asn	GTG Val 165	AAC Asn	GAG Glu	GGC Gly	TCC Ser	CAG Gln 170			576	
35	CAG Gln	AAA Lys	CTC Leu	TTC Phe	ACT Thr 175	GTG Val	GAG Glu	GCC Ala	ACA Thr	GCC Ala 180	AGG Arg	GTG Val	ACA Thr	CCC Pro	CGG Arg 185	AGC Ser			624	
40	TCA Ser	GAT Asp	AAT Asn	AGG Arg 190	CAG Gln	TTG Leu	CTG Leu	GTC Val	TGT Cys 195	GAG Glu	GCG Ala	TCT Ser	AGC Ser	CCA Pro 200	GCA Ala	CTG Leu			672	
45	GAG Glu	GCC Ala	CCC Pro 205	ATC Ile	AAG Lys	GCC Ala	TCA Ser 210	TTC Phe	ACC Thr	GTG Val	AAT Asn	GTT Val	CTG Leu 215	TTC Phe	CCT Pro	CCA Pro			720	
50	GGA Gly	CCC Pro 220	CCT Pro	GTC Val	ATC Ile	GAG Glu 225	TGG Trp	CCA Pro	GGC Gly	CTG Leu	GAT Asp 230	GAG Glu	GGG Gly	CAC His	GTG Val	CGG Arg			768	
55	GCA Ala 235	GGA Gly	CAG Gln	AGC Ser	TTG Leu 240	GAG Glu	CTG Leu	CCG Pro	TGC Cys	GTG Val	GCC Ala 245	CGA Arg	GGG Gly	GGT Gly	AAT Asn	CCC Pro 250			816	
60	TTA Leu	GCC Ala	ACA Thr	CTG Leu 255	CAG Gln	TGG Trp	CTG Leu	AAG Lys	AAT Asn	GGC Gly 260	CAG Gln	CCG Pro	GTG Val	TCC Ser	ACA Thr 265	GCG Ala			864	
65	TGG Trp	GGC Gly	ACA Thr	GAG Glu 270	CAC His	ACC Thr	CAG Gln	GCG Ala	GTG Val 275	GCC Ala	CGC Arg	AGT Ser	GTG Val	CTG Leu 280	GTG Val	ATG Met			912	
70	ACC Thr	GTG Val	AGG Arg 285	CCA Pro	GAA Glu	GAC Asp	CAT His 290	GGA Gly	GCG Ala	CAG Gln	CTC Leu	AGC Ser	TGC Cys 295	GAG Glu	GCC Ala	CAC His			960	



	CCA	ACT	AAC	GTG	ACG	ATC	CTG	GCC	AAC	GCA	TCC	GCA	CTG	CGC	CCG	GGA	1680
	Pro	Thr	Asn	Val	Thr	Ile	Leu	Ala	Asn	Ala	Ser	Ala	Leu	Arg	Pro	Gly	
			525					530					535				
5	GAC	GCC	TTA	AAC	TTG	ACA	TGC	GTC	AGC	GTC	AGC	AGC	AAT	CCG	CCG	GTC	1728
	Asp	Ala	Leu	Asn	Leu	Thr	Cys	Val	Ser	Val	Ser	Ser	Asn	Pro	Pro	Val	
		540					545					550					
10	AAC	TTG	TCC	TGG	GAC	AAG	GAA	GGG	GAG	AGG	CTG	GAG	GGC	GTG	GCC	GCC	1776
	Asn	Leu	Ser	Trp	Asp	Lys	Glu	Gly	Glu	Arg	Leu	Glu	Gly	Val	Ala	Ala	
		555				560					565					570	
15	CCA	CCC	CGG	AGA	GCC	CCA	TTC	AAA	GGC	TCC	GCC	GCC	GCC	AGG	AGC	GTC	1824
	Pro	Pro	Arg	Arg	Ala	Pro	Phe	Lys	Gly	Ser	Ala	Ala	Ala	Arg	Ser	Val	
					575					580					585		
20	CTT	CTG	CAA	GTG	TCA	TCC	CGC	GAT	CAT	GGC	CAG	CGC	GTG	ACC	TGC	CGC	1872
	Leu	Leu	Gln	Val	Ser	Ser	Arg	Asp	His	Gly	Gln	Arg	Val	Thr	Cys	Arg	
				590					595					600			
25	GCC	CAC	AGC	GCC	GAG	CTC	CGC	GAA	ACC	GTG	AGC	TCC	TTC	TAT	CGC	CTC	1920
	Ala	His	Ser	Ala	Glu	Leu	Arg	Glu	Thr	Val	Ser	Ser		Phe	Tyr	Arg	
			605				610						615				
30	AAC	GTA	CTG	TAC	CGT	CCA	GAG	TTC	CTG	GGG	GAG	CAG	GTG	CTG	GTG	GTG	1968
	Asn	Val	Leu	Tyr	Arg	Pro	Glu	Phe	Leu	Gly	Glu	Gln	Val	Leu	Val	Val	
		620					625					630					
35	ACC	GCG	GTG	GAG	CAG	GGC	GAG	GCG	TTG	CTG	CCC	GTG	TCC	GTG	TCC	GCT	2016
	Thr	Ala	Val	Glu	Gln	Gly	Glu	Ala	Leu	Leu	Pro	Val	Ser	Val	Ser	Ala	
		635				640					645					650	
40	AAC	CCC	GCC	CCC	GAG	GCC	TTC	AAC	TGG	ACC	TTC	CGC	GGC	TAT	CGC	CTC	2064
	Asn	Pro	Ala	Pro	Glu	Ala	Phe	Asn	Trp	Thr	Phe	Arg	Gly	Tyr	Arg	Leu	
				655					660					665			
45	AGT	CCA	GCG	GGC	GGC	CCC	CGG	CAT	CGC	ATC	CTG	TCC	AGC	GGG	GCT	CTG	2112
	Ser	Pro	Ala	Gly	Gly	Pro	Arg	His	Arg	Ile	Leu	Ser	Ser	Gly	Ala	Leu	
				670				675						680			
50	CAT	CTG	TGG	AAT	GTG	ACC	CGC	GCG	GAC	GAC	GGC	CTC	TAT	CAG	CTG	CAC	2160
	His	Leu	Trp	Asn	Val	Thr	Arg	Ala	Asp	Asp	Gly	Leu	Tyr	Gln	Leu	His	
			685				690						695				
55	TGC	CAG	AAC	TCT	GAG	GGC	ACC	GCG	GAA	GCG	CGG	CTG	CGG	CTG	GAC	GTG	2208
	Cys	Gln	Asn	Ser	Glu	Gly	Thr	Ala	Glu	Ala	Arg	Leu	Arg	Leu	Asp	Val	
		700				705					710						
60	CAC	TAT	GCT	CCC	ACC	ATC	CGT	GCC	CTC	CAG	GAC	CCC	ACT	GAG	GTG	AAC	2256
	His	Tyr	Ala	Pro	Thr	Ile	Arg	Ala	Leu	Gln	Asp	Pro	Thr	Glu	Val	Asn	
		715				720					725					730	
65	GTC	GGG	GGT	TCT	GTG	GAC	ATA	GTC	TGC	ACT	GTC	GAT	GCC	AAT	CCC	ATC	2304
	Val	Gly	Gly	Ser	Val	Asp	Ile	Val	Cys	Thr	Val	Asp	Ala	Asn	Pro	Ile	
				735					740							745	



	CCC CAG GCC ACC ACC TTC ACG CTG ACT GGT CTA CAG CCT TCT ACA AGA	3024
	Pro Gln Ala Thr Thr Phe Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg	
	975 980 985	
5	TAC AGG GTC TGG CTG CTG GCC AGT AAT GCC TTG GGG GAC AGT GGA CTG	3072
	Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly Leu	
	990 995 1000	
10	GCT GAC AAA GGG ACC CAG CTT CCC ATC ACT ACC CCA GGT CTC CAC CAG	3120
	Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu His Gln	
	1005 1010 1015	
15	CCT TCT GGA GAA CCT GAA GAC CAG CTG CCC ACA GAG CCA CCT TCA GGA	3168
	Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Glu Pro Pro Ser Gly	
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20	CCC TCG GGG CTG CCC CTG CTG CCT GTG CTG TTC GCT CTT GGG GGG CTT	3216
	Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala Leu Gly Gly Leu	
	1035 1040 1045 1050	
25	CTG CTC CTC TCC AAT GCC TCC TGT GTC GGG GGG GTC CTC TGG CAG CGG	3264
	Leu Leu Leu Ser Asn Ala Ser Cys Val Gly Gly Val Leu Trp Gln Arg	
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30	AGA CTC AGG CGT CTT GCT GAG GGC ATC TCA GAG AAG ACA GAG GCA GGG	3312
	Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser Glu Lys Thr Glu Ala Gly	
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35	TCG GAA GAG GAC CGA GTC AGG AAC GAA TAT GAG GAG AGC CAG TGG ACA	3360
	Ser Glu Glu Asp Arg Val Arg Asn Glu Tyr Glu Glu Ser Gln Trp Thr	
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40	GGA GAG CGG GAC ACT CAG AGC TCC ACG GTC AGC ACA ACA GAG GCA GAG	3408
	Gly Glu Arg Asp Thr Gln Ser Ser Thr Val Ser Thr Thr Glu Ala Glu	
	1100 1105 1110	
45	CCG TAT TAC CGC TCC CTG AGG GAC TTC AGC CCC CAG CTG CCC CCG ACG	3456
	Pro Tyr Tyr Arg Ser Leu Arg Asp Phe Ser Pro Gln Leu Pro Pro Thr	
	1115 1120 1125 1130	
50	CAG GAG GAG GTG TCT TAT TCC CGA GGT TTC ACA GGT GAA GAT GAG GAT	3504
	Gln Glu Glu Val Ser Tyr Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp	
	1135 1140 1145	
55	ATG GCC TTC CCT GGG CAC TTG TAT GAT GAG GTA GAA AGA ACG TAC CCC	3552
	Met Ala Phe Pro Gly His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro	
	1150 1155 1160	
60	CCG TCT GGA GCC TGG GGA CCC CTC TAC GAT GAA GTG CAG ATG GGA CCC	3600
	Pro Ser Gly Ala Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro	
	1165 1170 1175	
65	TGG GAC CTC CAC TGG CCT GAA GAC ACA TAT CAG GAT CCA AGA GGA ATC	3648
	Trp Asp Leu His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile	
	1180 1185 1190	

TAT GAC CAG GTG GCC GGA GAC TTG GAC ACT CTG GAA CCC GAT TCT CTG 3696  
 Tyr Asp Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu  
 1195 1200 1205 1210

5 CCC TTC GAG CTG AGG GGA CAT CTG GTG TAAGAGCCCT CTCAACCCCA 3743  
 Pro Phe Glu Leu Arg Gly His Leu Val  
 1215

10 TTGTCCTGCA CCTGCAGGAA TTTACACTCC ACTGGTCTCT CTCATTACAG CCTGGGCCGA 3803  
 GCTGGTTAGG TGAGCTCCAT AAAACCCAAA GGGACTTGGT GTCAGGAGAG GACATGGAGG 3863  
 GGGCTGAGTG ACAGAGATGG TTCAGCTGGT ACCAGAGTAG AAACAAGGTG CATCCTGGGG 3923

15 TTGGCTTTAG AAATAAACT TCTCCAAAAG GACAGGGCAG ATTGTAAACG TCGTCTCAAA 3983  
 AATGAAATGC TGCCGGGTGC GGTGACTCAC GCCTATAATC CCAGCACTTT GGGAGGCTGA 4043  
 GGCGGGTGGA TCACCTGAGG TCAGGAGTTC GAGACCAGCC TGGCCAACAT GGTAAAACTC 4103

20 CATTCTACT AAAAATATAA AAAATTAGCC AGGAGTAGTG GCGCATGCCT GTAGTCCCAG 4163  
 CTACTTGGA GGCTGATGCA TGAGAATTGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG 4223

25 CTGAGATCAC GCCACTGCAC TCCAGCCTGG GCGACAGAGC GAGATTCTGT CTCAAAAAAT 4283  
 AA 4285

30 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Ala Leu Gly Thr Thr Leu Arg Ala Ser Leu Leu Leu Gly Leu  
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45 Leu Thr Glu Gly Leu Ala Gln Leu Ala Ile Pro Ala Ser Val Pro Arg  
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Gly Phe Trp Ala Leu Pro Glu Asn Leu Thr Val Val Glu Gly Ala Ser  
 15 20 25

50 Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp  
 30 35 40

Ala Lys Asp Gly Leu Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe  
 45 50 55

55 Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu  
 60 65 70



His Ile Glu Ala Cys Asp Leu Ser Asp Asp Ala Glu Tyr Glu Cys Gln  
 75 80 85 90  
 5 Val Gly Arg Ser Glu Met Gly Pro Glu Leu Val Ser Pro Arg Val Ile  
 95 100 105  
 Leu Ser Ile Leu Val Pro Pro Lys Leu Leu Leu Leu Thr Pro Glu Ala  
 110 115 120  
 10 Gly Thr Met Val Thr Trp Val Ala Gly Gln Glu Tyr Val Val Asn Cys  
 125 130 135  
 Val Ser Gly Asp Ala Lys Pro Ala Pro Asp Ile Thr Ile Leu Leu Ser  
 140 145 150  
 15 Gly Gln Thr Ile Ser Asp Ile Ser Ala Asn Val Asn Glu Gly Ser Gln  
 155 160 165 170  
 20 Gln Lys Leu Phe Thr Val Glu Ala Thr Ala Arg Val Thr Pro Arg Ser  
 175 180 185  
 Ser Asp Asn Arg Gln Leu Leu Val Cys Glu Ala Ser Ser Pro Ala Leu  
 190 195 200  
 25 Glu Ala Pro Ile Lys Ala Ser Phe Thr Val Asn Val Leu Phe Pro Pro  
 205 210 215  
 Gly Pro Pro Val Ile Glu Trp Pro Gly Leu Asp Glu Gly His Val Arg  
 220 225 230  
 30 Ala Gly Gln Ser Leu Glu Leu Pro Cys Val Ala Arg Gly Gly Asn Pro  
 235 240 245 250  
 35 Leu Ala Thr Leu Gln Trp Leu Lys Asn Gly Gln Pro Val Ser Thr Ala  
 255 260 265  
 Trp Gly Thr Glu His Thr Gln Ala Val Ala Arg Ser Val Leu Val Met  
 270 275 280  
 40 Thr Val Arg Pro Glu Asp His Gly Ala Gln Leu Ser Cys Glu Ala His  
 285 290 295  
 Asn Ser Val Ser Ala Gly Thr Gln Glu His Gly Ile Thr Leu Gln Val  
 300 305 310  
 Thr Phe Pro Pro Ser Ala Ile Ile Ile Leu Gly Ser Ala Ser Gln Thr  
 315 320 325 330  
 50 Glu Asn Lys Asn Val Thr Leu Ser Cys Val Ser Lys Ser Ser Arg Pro  
 335 340 345  
 Arg Val Leu Leu Arg Trp Trp Leu Gly Trp Arg Gln Leu Leu Pro Met  
 350 355 360  
 55 Glu Glu Thr Val Met Asp Gly Leu His Gly Gly His Ile Ser Met Ser  
 365 370 375

	Asn	Leu	Thr	Phe	Leu	Ala	Arg	Arg	Glu	Asp	Asn	Gly	Leu	Thr	Leu	Thr	
	380						385					390					
5	Cys	Glu	Ala	Phe	Ser	Glu	Ala	Phe	Thr	Lys	Glu	Thr	Phe	Lys	Lys	Ser	
	395					400					405					410	
	Leu	Ile	Leu	Asn	Val	Lys	Tyr	Pro	Ala	Gln	Lys	Leu	Trp	Ile	Glu	Gly	
					415					420					425		
10	Pro	Pro	Glu	Gly	Gln	Lys	Leu	Arg	Ala	Gly	Thr	Arg	Val	Arg	Leu	Val	
				430					435					440			
	Cys	Leu	Ala	Ile	Gly	Gly	Asn	Pro	Glu	Pro	Ser	Leu	Met	Trp	Tyr	Lys	
15			445					450					455				
	Asp	Ser	Arg	Thr	Val	Thr	Glu	Ser	Arg	Leu	Pro	Gln	Glu	Ser	Arg	Arg	
	460						465					470					
20	Val	His	Leu	Gly	Ser	Val	Glu	Lys	Ser	Gly	Ser	Thr	Phe	Ser	Arg	Glu	
	475					480					485					490	
	Leu	Val	Leu	Val	Thr	Gly	Pro	Ser	Asp	Asn	Gln	Ala	Lys	Phe	Thr	Cys	
					495					500					505		
25	Lys	Ala	Gly	Gln	Leu	Ser	Ala	Ser	Thr	Gln	Leu	Ala	Val	Gln	Phe	Pro	
				510					515					520			
	Pro	Thr	Asn	Val	Thr	Ile	Leu	Ala	Asn	Ala	Ser	Ala	Leu	Arg	Pro	Gly	
30			525					530					535				
	Asp	Ala	Leu	Asn	Leu	Thr	Cys	Val	Ser	Val	Ser	Ser	Asn	Pro	Pro	Val	
	540						545					550					
35	Asn	Leu	Ser	Trp	Asp	Lys	Glu	Gly	Glu	Arg	Leu	Glu	Gly	Val	Ala	Ala	
	555					560					565					570	
	Pro	Pro	Arg	Arg	Ala	Pro	Phe	Lys	Gly	Ser	Ala	Ala	Ala	Arg	Ser	Val	
					575					580					585		
40	Leu	Leu	Gln	Val	Ser	Ser	Arg	Asp	His	Gly	Gln	Arg	Val	Thr	Cys	Arg	
				590					595					600			
	Ala	His	Ser	Ala	Glu	Leu	Arg	Glu	Thr	Val	Ser	Ser	Phe	Tyr	Arg	Leu	
45			605					610					615				
	Asn	Val	Leu	Tyr	Arg	Pro	Glu	Phe	Leu	Gly	Glu	Gln	Val	Leu	Val	Val	
							620		625			630					
50	Thr	Ala	Val	Glu	Gln	Gly	Glu	Ala	Leu	Leu	Pro	Val	Ser	Val	Ser	Ala	
	635					640					645					650	
	Asn	Pro	Ala	Pro	Glu	Ala	Phe	Asn	Trp	Thr	Phe	Arg	Gly	Tyr	Arg	Leu	
					655					660					665		
55	Ser	Pro	Ala	Gly	Gly	Pro	Arg	His	Arg	Ile	Leu	Ser	Ser	Gly	Ala	Leu	
				670					675					680			

His Leu Trp Asn Val Thr Arg Ala Asp Asp Gly Leu Tyr Gln Leu His  
 685 690 695

5 Cys Gln Asn Ser Glu Gly Thr Ala Glu Ala Arg Leu Arg Leu Asp Val  
 700 705 710

His Tyr Ala Pro Thr Ile Arg Ala Leu Gln Asp Pro Thr Glu Val Asn  
 715 720 725 730

10 Val Gly Gly Ser Val Asp Ile Val Cys Thr Val Asp Ala Asn Pro Ile  
 735 740 745

Leu Pro Gly Met Phe Asn Trp Glu Arg Leu Gly Glu Asp Glu Glu Asp  
 750 755 760

Gln Ser Leu Asp Asp Met Glu Lys Ile Ser Arg Gly Pro Thr Gly Arg  
 765 770 775

20 Leu Arg Ile His His Ala Lys Leu Ala Gln Ala Gly Ala Tyr Gln Cys  
 780 785 790

Ile Val Asp Asn Gly Val Ala Pro Pro Ala Arg Arg Leu Leu Arg Leu  
 795 800 805 810

25 Val Val Arg Phe Ala Pro Gln Val Glu His Pro Thr Pro Leu Thr Lys  
 815 820 825

Val Ala Ala Ala Gly Asp Ser Thr Ser Ser Ala Thr Leu His Cys Arg  
 830 835 840

Ala Arg Gly Val Pro Asn Ile Val Phe Thr Trp Thr Lys Asn Gly Val  
 845 850 855

35 Pro Leu Asp Leu Gln Asp Pro Arg Tyr Thr Glu His Thr Tyr His Gln  
 860 865 870

Gly Gly Val His Ser Ser Leu Leu Thr Ile Ala Asn Val Ser Ala Ala  
 875 880 885 890

40 Gln Asp Tyr Ala Leu Phe Thr Cys Thr Ala Thr Asn Ala Leu Gly Ser  
 895 900 905

Asp Gln Thr Asn Ile Gln Leu Val Ser Ile Ser Arg Pro Asp Pro Pro  
 910 915 920

Ser Gly Leu Lys Val Val Ser Leu Thr Pro His Ser Val Gly Leu Glu  
 925 930 935

50 Trp Lys Pro Gly Phe Asp Gly Gly Leu Pro Gln Arg Phe Cys Ile Arg  
 940 945 950

Tyr Glu Ala Leu Gly Thr Pro Gly Phe His Tyr Val Asp Val Val Pro  
 955 960 965 970

55 Pro Gln Ala Thr Thr Phe Thr Leu Thr Gly Leu Gln Pro Ser Thr Arg  
 975 980 985

Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly Leu  
 990 995 1000  
 5 Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu His Gln  
 1005 1010 1015  
 Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Glu Pro Pro Ser Gly  
 1020 1025 1030  
 10 Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala Leu Gly Gly Leu  
 1035 1040 1045 1050  
 Leu Leu Leu Ser Asn Ala Ser Cys Val Gly Gly Val Leu Trp Gln Arg  
 15 1055 1060 1065  
 Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser Glu Lys Thr Glu Ala Gly  
 1070 1075 1080  
 20 Ser Glu Glu Asp Arg Val Arg Asn Glu Tyr Glu Glu Ser Gln Trp Thr  
 1085 1090 1095  
 Gly Glu Arg Asp Thr Gln Ser Ser Thr Val Ser Thr Thr Glu Ala Glu  
 1100 1105 1110  
 25 Pro Tyr Tyr Arg Ser Leu Arg Asp Phe Ser Pro Gln Leu Pro Pro Thr  
 1115 1120 1125 1130  
 Gln Glu Glu Val Ser Tyr Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp  
 30 1135 1140 1145  
 Met Ala Phe Pro Gly His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro  
 1150 1155 1160  
 35 Pro Ser Gly Ala Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro  
 1165 1170 1175  
 Trp Asp Leu His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile  
 1180 1185 1190  
 40 Tyr Asp Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu  
 1195 1200 1205 1210  
 Pro Phe Glu Leu Arg Gly His Leu Val  
 45 1215

(2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "primer exon 2 5'UTR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 GAGAAAGCCA GACAGACGCA G

21

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer intron 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20 AGCTTCCGCT GGTGGCT

17

(2) INFORMATION FOR SEQ ID NO:5:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer intron 23"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCGGGGAGA CCCACCC

17

(2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer intron 26"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55 CCTGATGCTA ACGGCAGGGC

20